

What is claimed is:

Claim 1. An isolated DNA molecule encoding senescence-induced deoxyhypusine synthase, wherein the DNA molecule hybridizes under low stringency conditions with SEQ ID NO:1 and/or SEQ ID NO:9, or a functional derivative of the isolated DNA molecule which hybridizes with SEQ ID NO:1 and/or SEQ ID NO: 9 with the proviso that the DNA molecule does not have the sequence of SEQ ID NO:5.

Claim 2. The isolated DNA molecule of claim 1 wherein the DNA molecule has the nucleotide sequence of SEQ ID NO:1 or SEQ ID NO:9.

Claim 3. An isolated senescence-induced deoxyhypusine synthase encoded by a nucleotide sequence which hybridizes under low stringency conditions with SEQ ID NO:1 and/or SEQ ID NO:9, or a functional derivative of the senescence-induced deoxyhypusine synthase.

Claim 4. The senescence-induced deoxyhypusine synthase of claim 3 wherein the deoxyhypusine synthase has the amino acid sequence SEQ ID NO:2 or SEQ ID NO:10.

Claim 5. An isolated DNA molecule encoding senescence-induced eIF-5A, wherein the DNA molecule hybridizes under low stringency conditions with SEQ ID NO:11, SEQ ID NO:13 and/or SEQ ID NO:15, or a functional derivative of the isolated DNA molecule which hybridizes with SEQ ID NO:11, SEQ ID NO:13 and/or SEQ ID NO:15.

Claim 6. The isolated DNA molecule of claim 5 wherein the DNA molecule has the nucleotide sequence of SEQ ID NO:11, SEQ ID NO:13 or SEQ ID NO:15.

Claim 7. A vector for transformation of plant cells comprising
(a) antisense nucleotide sequences substantially complementary to (1) a corresponding portion of one strand of a DNA molecule encoding senescence-induced deoxyhypusine synthase wherein the DNA molecule encoding senescence-

induced deoxyhypusine synthase hybridizes under low stringency conditions with SEQ ID NO:1, SEQ ID NO:5 and/or SEQ ID NO:9 or (2) a corresponding portion of an RNA sequence encoded by the DNA molecule encoding senescence-induced deoxyhypusine synthase; and

(b) regulatory sequences operatively linked to the antisense nucleotide sequences such that the antisense nucleotide sequences are expressed in a plant cell into which it is transformed.

Claim 8. The vector according to claim 7 wherein the regulatory sequences comprise a promoter and a transcription termination region.

Claim 9. The vector according to claim 7 wherein the regulatory sequences comprise a constitutive promoter.

Claim 8. The vector according to claim 7 wherein the regulatory sequences comprise a plant tissue-specific promoter.

Claim 9. The vector according to claim 7 wherein the regulatory sequences comprise a senescence-induced plant promoter.

Claim 10. The vector according to claim 7 wherein the regulatory sequences comprise a viral promoter.

Claim 11. The vector according to claim 10 wherein the regulatory sequences further comprise a constitutive promoter.

~~Claim 12. The vector according to claim 7 further comprising (a) antisense nucleotide sequences substantially complementary to (1) a corresponding portion of one strand of a DNA molecule encoding senescence-induced eIF-5A wherein the DNA molecule encoding senescence-induced eIF-5A hybridizes under low stringency conditions with SEQ ID NO:11, SEQ ID NO:13 and/or SEQ ID NO:15 or (2) a corresponding portion of an RNA sequence encoded by the DNA molecule encoding~~

senescence-induced eIF-5A; and

(b) regulatory sequences operatively linked to the antisense nucleotide sequences such that the antisense nucleotide sequences are expressed in a plant cell into which it is transformed.

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Claim 13 . A vector for transformation of plant cells comprising

(a) antisense nucleotide sequences substantially complementary to (1) a corresponding portion of one strand of a DNA molecule encoding senescence-induced eIF-5A wherein the DNA molecule encoding senescence-induced eIF-5A hybridizes under low stringency conditions with SEQ ID NO:11, SEQ ID NO:13 and/or SEQ ID NO:15 or (2) a corresponding portion of an RNA sequence encoded by the DNA molecule encoding senescence-induced eIF-5A; and

(b) regulatory sequences operatively linked to the nucleotide sequences such that the antisense nucleotide sequences are expressed in a plant cell into which it is transformed.

Claim 14. An antisense oligonucleotide or polynucleotide encoding an RNA molecule which is substantially complementary to (i) a corresponding portion of an RNA transcript of a plant senescence-induced deoxyhypusine synthase gene, wherein said plant gene hybridizes under low stringency conditions with SEQ ID NO:1, SEQ ID NO:5 and/or SEQ ID NO:9 or (ii) a corresponding portion of an RNA transcript of a plant senescence-induced eIF-5A gene, wherein said plant gene hybridizes under low stringency conditions with SEQ ID NO:11, SEQ ID NO:13 and/or SEQ ID NO:15.

Claim 15. The antisense oligonucleotide or polynucleotide according to claim 14 wherein the oligonucleotide or polynucleotide comprises about six to about 100 nucleotides.

Claim 16. The antisense oligonucleotide or polynucleotide according to claim 14 wherein the antisense oligonucleotide or polynucleotide is substantially complementary to a corresponding portion of the 5'-non-coding region of the RNA

transcript.

Claim 17. The antisense oligonucleotide or polynucleotide according to claim 14 wherein the antisense oligonucleotide or polynucleotide is substantially complementary to a corresponding portion of the 3'-end of the RNA transcript.

Claim 18. The antisense oligonucleotide or polynucleotide according to claim 14 wherein the antisense oligonucleotide or polynucleotide is substantially complementary to the 3'-end of *Arabidopsis* senescence-induced DHS gene.

Claim 19. The antisense oligonucleotide or polynucleotide according to claim 17 wherein the antisense oligonucleotide or polynucleotide is substantially complementary to SEQ ID NO:23.

Claim 20. The antisense oligonucleotide or polynucleotide according to claim 17 wherein the antisense oligonucleotide or polynucleotide is substantially complementary to SEQ ID NO:30.

Claim 21. A vector comprising a DNA molecule encoding
(a) senescence-induced deoxyhypusine synthase, wherein the DNA molecule hybridizes under low stringency conditions with SEQ ID NO:1, SEQ ID NO:5, and/or SEQ ID NO:9; and

(b) regulatory sequences operatively linked to the DNA molecule such that the deoxyhypusine synthase is expressed in a plant cell into which it is transformed.

Claim 22. A vector comprising a DNA molecule encoding
(a) senescence-induced eIF-5A, wherein the DNA molecule hybridizes under low stringency conditions with SEQ ID NO:11, SEQ ID NO:13, and/or SEQ ID NO:15; and

(b) regulatory sequences operatively linked to the DNA molecule such that eIF-5A is expressed in a plant cell into which it is transformed.

Claim 23. A vector comprising a DNA molecule encoding

(a) senescence-induced deoxyhypusine synthase, wherein the DNA molecule hybridizes under low stringency conditions with SEQ ID NO:1, SEQ ID NO:5, and/or SEQ ID NO:9;

(b) senescence-induced eIF-5A, wherein the DNA molecule hybridizes under low stringency conditions with SEQ ID NO:11, SEQ ID NO:13, and/or SEQ ID NO:15; and

(b) regulatory sequences operatively linked to the DNA molecule such that the senescence-induced deoxyhypusine synthase and the eIF-5A are expressed in a plant cell into which it is transformed.

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Claim 24. A bacterial cell transformed with the vector according to any one of claims 7, 12 or 13.

Claim 25. A plant cell transformed with the vector according to any one of claims 7, 12 or 13.

Claim 26. A plant and progeny thereof, wherein the plant is generated from a plant cell transformed with the vector according to any one of claims 7, 12 or 13.

Claim 27. A plant part derived from a plant or progeny according to claim 26.

Claim 28. A method for inhibiting the expression of endogenous senescence-induced deoxyhypusine synthase, eIF-5A or both in a plant, said method comprising

(1) integrating into the genome of the plant a vector comprising

(A) antisense nucleotide sequences substantially complementary to (i) a corresponding portion of one strand of a DNA molecule encoding the endogenous senescence-induced deoxyhypusine synthase, wherein the DNA molecule encoding the endogenous senescence-induced deoxyhypusine synthase hybridizes with SEQ ID NO:1, SEQ ID NO:5, and/or SEQ ID NO:9 or (ii) a corresponding portion of an RNA sequence encoded by the endogenous senescence-induced deoxyhypusine synthase gene, (iii) a corresponding portion of one strand of a DNA molecule

encoding the endogenous senescence-induced eIF-5A, wherein the DNA molecule encoding the endogenous senescence-induced deoxyhypusine synthase hybridizes with SEQ ID NO:11, SEQ ID NO:13, and/or SEQ ID NO:15, (iv) a corresponding portion of an RNA sequence encoded by the endogenous senescence-induced eIF-5A, or (v) a combination of (i) or (ii) and (iii) or (iv); and

(B) regulatory sequences operatively linked to the antisense nucleotide sequences such that the antisense nucleotide sequences are expressed; and

(2) growing said plant, whereby said antisense nucleotide sequences are transcribed and bind to said RNA sequence, whereby expression of the senescence-induced deoxyhypusine synthase gene, senescence-induced eIF-5A gene or both is inhibited.

Claim 29. The method according to claim 28 wherein the portion of the DNA or the portion of the RNA to which the antisense nucleotide sequence is substantially complementary comprises 5'-non-coding or 3'-coding and/or non-coding sequences.

Claim 30. The method according to claim 28 wherein the antisense nucleotide sequence is substantially complementary to SEQ ID NO:23

Claim 31. The method according to claim 28 wherein the antisense nucleotide sequence is substantially complementary to SEQ ID NO:30.

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013 Claim 32. The method according to claim 28 wherein said inhibition results in altered senescence of the plant.

Claim 33. The method according to claim 28 wherein said inhibition results in increased resistance of said plant to environmental stress-induced and/or pathogen-induced senescence.

Claim 34. The method according to claim 28 wherein said inhibition results in increased biomass of said plant.

Claim 35. The method according to claim 28 wherein said inhibition results in delayed fruit softening and spoilage in said plant.

Claim 36. The method according to claim 28 wherein said inhibition results in increased seed yield from said plant.

Claim 37. The method according to claim 28 wherein the regulatory sequences comprise a constitutive promoter active in the plant.

Claim 38. The method according to claim 28 wherein the regulatory sequences comprise a tissue specific promoter active in the plant.

Claim 39. The method according to claim 28 wherein the regulatory sequences comprise a senescence-induced promoter active in the plant.

Claim 40. The method according to claim 28 wherein said plant is selected from the group consisting of fruit bearing plants, flowering plants, vegetables, agronomic crop plants and forest species.

Claim 41. The method according to claim 28 wherein the plant is a tomato.

Claim 42. The method according to claim 28 wherein the plant is a flowering plant.

Claim 43. A method for inhibiting the expression of an endogenous senescence-induced deoxyhypusine synthase gene in a plant cell, said method comprising

(1) integrating into the genome of at least one cell of the plant a vector comprising

(A) an isolated DNA molecule encoding exogenous senescence-induced deoxyhypusine synthase, wherein the DNA molecule hybridizes under low stringency conditions with SEQ ID NO:1, SEQ ID NO:5, and/or SEQ ID NO:9 or a

functional derivative of the isolated DNA molecule which hybridizes with SEQ ID:1, SEQ ID NO:5, and/or SEQ ID NO:9; and

(B) regulatory sequences operatively linked to the DNA molecule such that the exogenous senescence-induced deoxyhypusine synthase encoded thereby is expressed; and

(2) growing said plant, whereby said DNA molecule is over-expressed and the endogenous senescence-induced deoxyhypusine synthase gene is inhibited by exogenous senescence-induced deoxyhypusine synthase.

Claim 44. The method according to claim 43 wherein the regulatory sequences comprise a constitutive promoter.

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Out Claim 45. A method of altering age-related senescence and/or environmental stress-related senescence in a plant, said method comprising

(1) integrating into the genome of the plant a vector comprising

(A) antisense nucleotide sequences substantially complementary to (i) a corresponding portion of one strand of a DNA molecule encoding the endogenous senescence-induced deoxyhypusine synthase, wherein the DNA molecule encoding the endogenous senescence-induced deoxyhypusine synthase hybridizes with SEQ ID NO:1, SEQ ID NO: 5 and/or SEQ ID NO:9 or (ii) at least a portion of an RNA sequence encoded by the endogenous senescence-induced deoxyhypusine synthase gene, (iii) a corresponding portion of one strand of a DNA molecule encoding the endogenous senescence-induced eIF-5A gene, wherein the DNA molecule encoding the endogenous senescence-induced eIF-5A hybridizes with SEQ ID NO:11, SEQ ID NO:13 and/or SEQ ID NO:15, (iv) a corresponding portion of an RNA sequence encoded by the endogenous senescence-induced eIF-5A gene, or (v) a combination of (i) or (ii) and (iii) or (iv);

(B) regulatory sequences operatively linked to the antisense nucleotide sequences such that the antisense nucleotide sequences are expressed; and

(2) growing said plant, whereby said antisense nucleotide sequences are transcribed and bind to said RNA sequence, whereby expression of said senescence-induced deoxyhypusine synthase gene, senescence-induced eIF-5A

gene or both is inhibited.

Claim 46. A transgenic plant cell comprising a vector according to any one of claims 7, 12, 13 or a combination of said vectors.

Claim 47. A transgenic plant cell comprising a vector according to any one of claims 21, 22, 23 or a combination of said vectors.

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us Claim 48. A plasmid comprising a replication system functional in a prokaryotic host and an antisense oligonucleotide or polynucleotide according to claim 14.

Claim 49. A plasmid comprising a replication system functional in *Agrobacterium* and an antisense oligonucleotide or polynucleotide according to claim 14.

Claim 50. A plant and progeny thereof, wherein said plant is derived from a cell having inhibited or reduced expression of senescence-induced deoxyhypusine synthase, senescence-induced eIF-5A or both, said cell comprising a vector according to any one of claims 7, 12 or 13.

Claim 51. A plant and progeny thereof, wherein said plant is derived from a cell having inhibited or reduced expression of senescence-induced deoxyhypusine synthase, senescence-induced eIF-5A, or both, wherein said cell is produced by

- (1) integrating into the genome of the cell a vector comprising
 - (A) antisense nucleotide sequences substantially complementary to (i) a corresponding portion of one strand of a DNA molecule encoding the endogenous senescence-induced deoxyhypusine synthase, wherein the DNA molecule encoding the endogenous senescence-induced deoxyhypusine synthase hybridizes with SEQ ID NO:1, SEQ ID NO: 5, and/or SEQ ID NO:9 or (ii) a corresponding portion of an RNA sequence encoded by the endogenous senescence-induced deoxyhypusine synthase gene, (iii) a corresponding portion of one strand of a DNA molecule

encoding the endogenous senescence-induced eIF-5A gene, wherein the DNA molecule encoding the endogenous senescence-induced eIF-5A hybridizes with SEQ ID NO:11, SEQ ID NO:13 and/or SEQ ID NO:15, (iv) a corresponding portion of an RNA sequence encoded by the endogenous senescence-induced eIF-5A gene, or (v) a combination of (I) or (ii) and (iii) or (iv); and

(B) regulatory sequences operatively linked to the antisense nucleotide sequences such that the antisense nucleotides are expressed; and

(2) growing said cell, whereby said antisense nucleotide sequences are transcribed and bind to said RNA sequence, whereby expression of said senescence-induced deoxyhypusine synthase gene, senescence-induced eIF-5A gene or both is inhibited.

Claim 52. The plant and progeny according to claim 51 wherein the plant is a tomato.

Claim 53. The plant and progeny according to claim 52 wherein the plant is a flowering plant.

Claim 54. A method of inhibiting seed aging, said method comprising

(1) integrating into the genome of a plant a vector comprising

(A) antisense nucleotide sequences substantially complementary to

(i) a corresponding portion of one strand of a DNA molecule encoding an endogenous aging-induced deoxyhypusine synthase, wherein DNA encoding said endogenous aging-induced deoxyhypusine synthase hybridizes with SEQ ID NO:1, SEQ ID NO:5 and/or SEQ ID NO:9 or (ii) a corresponding portion of an RNA sequence transcribed from a DNA molecule encoding an endogenous senescence-induced deoxyhypusine synthase gene; and

(B) regulatory sequences operatively linked to the antisense nucleotide sequences; and

(2) growing said plant, whereby said antisense nucleotide sequences are transcribed and bind to said RNA sequence and expression of said aging-induced deoxyhypusine synthase gene is inhibited.

Claim 55. The method according to claim 54 further comprising integrating into the genome of a plant a vector comprising

- (A) antisense nucleotide sequences substantially complementary to
 - (i) a corresponding portion of one strand of a DNA molecule encoding an endogenous aging-induced eIF-5A gene, wherein DNA encoding said endogenous aging-induced eIF-5A hybridizes with SEQ ID NO:11, SEQ ID NO:13 and/or SEQ ID NO:15 or
 - (ii) a corresponding portion of an RNA sequence transcribed from a DNA molecule encoding an endogenous senescence-induced eIF-5A gene; and
- (B) regulatory sequences operatively linked to the antisense nucleotide sequences.

Claim 56. A method of inhibiting seed aging, said method comprising

- (1) integrating into the genome of a plant a vector comprising
 - (A) antisense nucleotide sequences substantially complementary to
 - (i) a corresponding portion of one strand of a DNA molecule encoding an endogenous aging-induced deoxyhypusine synthase, wherein DNA encoding said endogenous aging-induced deoxyhypusine synthase hybridizes with SEQ ID NO:1, SEQ ID NO:5 and/or SEQ ID NO:9 or
 - (ii) a corresponding portion of a substantially complementary RNA sequence transcribed from a DNA molecule encoding an endogenous senescence-induced deoxyhypusine synthase gene, (iii) a corresponding portion of one strand of a DNA molecule encoding an endogenous aging-induced eIF-5A gene, wherein DNA encoding said endogenous aging-induced eIF-5A hybridizes with SEQ ID NO:11, SEQ ID NO:13 and/or SEQ ID NO:15 , (iv) a corresponding portion of a substantially complementary RNA sequence transcribed from a DNA molecule encoding an endogenous senescence-induced eIF-5A gene; or
 - (v) a combination of (i) or (ii) and (iii) or (iv); and
 - (B) regulatory sequences operatively linked to the antisense nucleotide sequences; and
- (2) growing said plant, whereby said antisense nucleotide sequences are transcribed and bind to said substantially complementary RNA sequence and expression of said aging-induced deoxyhypusine synthase gene, eIF-5A gene or both is inhibited.

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Claim 57. A method of increasing seed yield from a plant, said method comprising

- (1) integrating into the genome of the plant a vector comprising
 - (A) antisense nucleotide sequences substantially complementary to
 - (i) a corresponding portion of one strand of a DNA molecule encoding an endogenous senescence-induced deoxyhypusine synthase, wherein DNA encoding said endogenous senescence-induced deoxyhypusine synthase hybridizes with SEQ ID NO:1, SEQ ID NO:5 and/or SEQ ID NO:9 or
 - (ii) a corresponding portion of an RNA sequence transcribed from a DNA molecule encoding an endogenous senescence-induced deoxyhypusine synthase gene; and
 - (B) regulatory sequences operatively linked to the antisense nucleotide sequences; and
- (2) growing said plant, whereby said antisense nucleotide sequences are transcribed and bind to said RNA sequence and expression of said deoxyhypusine synthase gene is inhibited.

~~Claim 58. The method according to claim 57 further comprising integrating into the genome of a plant a vector comprising~~

- ~~(A) antisense nucleotide sequences substantially complementary to~~
 - ~~(i) a corresponding portion of one strand of a DNA molecule encoding an endogenous aging-induced eIF-5A gene, wherein DNA encoding said endogenous aging-induced eIF-5A hybridizes with SEQ ID NO:11, SEQ ID NO:13 and/or SEQ ID NO:15 or~~
 - ~~(ii) a corresponding portion of an RNA sequence transcribed from a DNA molecule encoding an endogenous senescence-induced eIF-5A gene; and~~
- ~~(B) regulatory sequences operatively linked to the antisense nucleotide sequences.~~

Claim 59. A vector for transformation of plant cells comprising

- (a) antisense nucleotide sequences substantially complementary to (1) a corresponding portion of one strand of a DNA molecule encoding a 3' portion of senescence-induced deoxyhypusine synthase wherein the DNA molecule encoding

senescence-induced deoxyhypusine synthase hybridizes under low stringency conditions with SEQ ID NO:31 or (2) a corresponding portion of an RNA sequence encoded by the DNA molecule encoding the 3' portion of senescence-induced deoxyhypusine synthase; and

(b) regulatory sequences operatively linked to the antisense nucleotide sequences such that the antisense nucleotide sequences are expressed in a plant cell into which it is transformed.

Claim 60. The vector according to claim 59 wherein the regulatory sequences comprise a promoter and a transcription termination region.

Claim 61. The vector according to claim 59 wherein the regulatory sequences comprise a constitutive promoter.

Claim 62. The vector according to claim 59 wherein the regulatory sequences comprise a plant tissue-specific promoter.

Claim 63. The vector according to claim 59 wherein the regulatory sequences comprise a senescence-induced plant promoter.

Claim 64. The vector according to claim 59 wherein the regulatory sequences comprise a viral promoter.

Claim 65. The vector according to claim 59 wherein the regulatory sequences further comprise a constitutive promoter.

Claim 66. The vector according to claim 59 further comprising (a) antisense nucleotide sequences substantially complementary to (1) a corresponding portion of one strand of a DNA molecule encoding senescence-induced eIF-5A wherein the DNA molecule encoding senescence-induced eIF-5A hybridizes under low stringency conditions with SEQ ID NO:11, SEQ ID NO:13 and/or SEQ ID NO:15 or (2) a corresponding portion of an RNA sequence encoded by the DNA molecule encoding

senescence-induced eIF-5A; and

(b) regulatory sequences operatively linked to the antisense nucleotide sequences such that the antisense nucleotide sequences are expressed in a plant cell into which it is transformed.

Claim 67. A method of increasing resistance to physiological disease in a plant, said method comprising

(1) integrating into the genome of the plant a vector comprising

(A) antisense nucleotide sequences substantially complementary to (i) a corresponding portion of one strand of a DNA molecule encoding the 3' end of endogenous senescence-induced deoxyhypusine synthase, wherein the DNA molecule encoding the endogenous senescence-induced deoxyhypusine synthase hybridizes with SEQ ID NO:31 or (ii) at least a portion of an RNA sequence encoded by the 3' end of the endogenous senescence-induced deoxyhypusine synthase gene, (iii) a corresponding portion of one strand of a DNA molecule encoding the endogenous senescence-induced eIF-5A gene, wherein the DNA molecule encoding the endogenous senescence-induced eIF-5A hybridizes with SEQ ID NO:11, SEQ ID NO:13 and/or SEQ ID NO:15, (iv) a corresponding portion of an RNA sequence encoded by the endogenous senescence-induced eIF-5A gene, or (v) a combination of (i) or (ii) and (iii) or (iv);

(B) regulatory sequences operatively linked to the antisense nucleotide sequences such that the antisense nucleotide sequences are expressed; and

(2) growing said plant, whereby said antisense nucleotide sequences are transcribed and bind to said RNA sequence, whereby expression of said senescence-induced deoxyhypusine synthase gene, senescence-induced eIF-5A gene or both is inhibited.

Claim 68. The method of claim 67, wherein said disease is blossom end rot.

Claim 69. A plant and progeny thereof, wherein said plant is derived from a cell having inhibited or reduced expression of senescence-induced deoxyhypusine synthase, senescence-induced eIF-5A, or both, wherein said cell is produced by

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- (1) integrating into the genome of the cell a vector comprising
- (A) antisense nucleotide sequences substantially complementary to (i) a corresponding portion of one strand of a DNA molecule encoding the 3' end of the endogenous senescence-induced deoxyhypusine synthase, wherein the DNA molecule encoding the endogenous senescence-induced deoxyhypusine synthase hybridizes with SEQ ID NO:31 or (ii) a corresponding portion of an RNA sequence encoded by the 3' end of the endogenous senescence-induced deoxyhypusine synthase gene, (iii) a corresponding portion of one strand of a DNA molecule encoding the endogenous senescence-induced eIF-5A gene, wherein the DNA molecule encoding the endogenous senescence-induced eIF-5A hybridizes with SEQ ID NO:11, SEQ ID NO:13 and/or SEQ ID NO:15, (iv) a corresponding portion of an RNA sequence encoded by the endogenous senescence-induced eIF-5A gene, or (v) a combination of (i) or (ii) and (iii) or (iv); and
 - (B) regulatory sequences operatively linked to the antisense nucleotide sequences such that the antisense nucleotides are expressed; and
- (2) growing said cell, whereby said antisense nucleotide sequences are transcribed and bind to said RNA sequence, whereby expression of said senescence-induced deoxyhypusine synthase gene, senescence-induced eIF-5A gene or both is inhibited.

Claim 70. The plant and progeny according to claim 69 wherein the plant is a tomato.

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